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score greater than or equal to the score of the result being printed,
 and is derived by analysis of the total score distribution.

SUMMARIES

OM nucleic - nucleic search, using sw model					
Run on:	April 26, 2003, 15:58:54 ; Search time 2917 Seconds (without alignments) 1563.834 Million cell updates/sec				
Title:	US-09-836-960-4				
Perfect score:	1570				
Sequence:	ccccacgcgtccgcgacgcaaaaaaaaaaaaaaaa 1570				
Scoring table:	IDENTITY_NUC				
	Gapop 10.0 , Gapext 1.0				
Searched:	2054640 seqs, 14551402878 residues				
Total number of hits satisfying chosen parameters:	4109280				
Minimum DB seq length:	0				
Maximum DB seq length:	2000000000				
Post-processing:	Minimum Match 0%				
	Listing first 45 summaries				
Database :					
1: gb_ba:*					
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5: gb_ov:*					
6: gb_stc:*					
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12: gb_sy:*					
13: gb_un:*					
14: gb_vl:*					
15: en_ba:*					
16: en_fun:*					
17: en_hum:*					
18: en_in:*					
19: en_mu:*					
20: en_on:*					
21: en_or:*					
22: en_ov:*					
23: en_pat:*					
24: en_ph:*					
25: en_pl:*					
26: en_ro:*					
27: en_sis:*					
28: en_vl:*					
29: en_vt:*					
30: en_htg_hum:*					
31: en_htg_inv:*					
32: en_htg_other:*					
33: en_htg_mus:*					
34: en_htg_pln:*					
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41: en_htgo_other:*					

Pred. No. is the number of results predicted by chance to have a

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DEFINITION	Homo sapiens, fibroblast				
Db	547	GCGCCCTGGCCGACTTGCCCTGTGTTTACACTTCCTGCTGCTGTCTTCAGGTACAG	606		
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QY	679	CGGGACGATGTTGAGCCGTAAGCACTGCTGGCTGTACAGCTACAGCCGACAGTGG	738		
Db	667	CGGAGCGTGTGAGCCGTAAGCACTGCTGGCTGTACAGCTACAGCCGACAGTGG	726		
QY	739	AAACACATCAGTCTCCCTGGGCCAGATCACTAGCTGCGCGGAGGAGAACGAGA	798		
Db	727	AAACACATCAGTCTCCCTGGGCCAGATCACTAGCTGCGCGGAGGAGAACGAGA	786		
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Db	787	GCCAGCTCTAGTGGAGACAGACACCTTCTGGTAGTCAGTCGCGATCAAGGAG	846		
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Db	847	ACCGAATCTTACCTGTGATGACCGCAAGCTGCTGGGAAGCCGATGCGACC	906		
QY	919	ACCAAGGAGTGTGTGTATCCAGAAGTCTGGAGACAACTACAGGCCCTGATG	978		
Db	907	ACCAAGGAGTGTGTGTATCCAGAAGTCTGGAGACAACTACAGGCCCTGATG	966		
QY	979	GCTAAGTACTCCCGCTGTACGTGGCTTACCAAGAGGGGGGGAGGGCCC	1038		
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QY	1159	AACACCCCTGCCTAGGCACCCGGCGCCGCGCCCTAGGTGCCCTGGCCACACTCAC	1218		
Db	1147	AACACCCCTGCCTAGGCACCCGGCGCCGCGCCCTAGGTGCCCTGGCCACACTCAC	1206		
QY	1219	TCCCCAGAAACATGCACTAGAGAATAATTTCATGAAATAAGGAGAGCTCPATT	1278		
Db	1207	TCCCCAGAAACATGCACTAGAGAATAATTTCATGAAATAAGGAGAGCTCPATT	1266		
QY	1279	TGTACATTGTTAAAGAGACAAACTGACCAAAACTCTGGGGAGGGTGAA	1338		
Db	1267	TGTACATTGTTAAAGAGACAAACTGACCAAAACTCTGGGGAGGGTGAA	1326		
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Db	1327	TAAGGATTTATGTTGACCTGAAACCCCGATGACAACAAACTCACGAAAGGACTGT	1386		
QY	1399	AGTCACCCACAGGTCTTGCTCTGTGTTAGAACAGACAACTCTGGGGAGGGTGAA	1458		
Db	1387	AGTCACCCACAGGTCTTGCTCTGTGTTAGAACAGACAACTCTGGGGAGGGTGAA	1446		
QY	1459	GGAGGACTTGTAGTGGAAACCAACACTTGAGAACCCAAGTCCTTTCCCAAAGGT	1518		
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QY	1519	CTGAAGAGAAAAAAACACAAAAAAACACAAAAAAACACAAAAAAACACAAAAAA	1558		
Db	1507	CTGAAGAGAAAAAAACACAAAAAAACACAAAAAAACACAAAAAAACACAAAAAA	1546		

ACCESSION VERSION	SOURCE	ORGANISM	IMAGE:3948893, mRNA, complete cds.
KEYWORDS		Homo sapiens	
B006245		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.	
B006245.1			
MGCC			
REMARK	COMMENT		
	Email: cgap@r@mail.nih.gov		
	Tissue Procurement: DCTD/DPR		
	cDNA Library Preparation: Rubin Laboratory		
	cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)		
	DNA Sequencing by: National Institutes of Health Intramural Sequencing Center (NISC), Gaithersburg, Maryland;		
	Contact: MGC help desk nih.gv		
	Web site: http://www.nisc.nih.gov/		
	Contact: nisc-mgc@nigri.nih.gov		
	Shevchenko, V., Wetherby, K.D., Beckstrom-Sternberg, S.M., Benjamin, B., Blakesley, R.W., Bouffard, G.G., Brinkley, C., Brooks, S., Dietrich, N.L., Guan, X., Gupta, J., Ho, S.-L., Karins, E., Legaspi, R., Lim, M., Maduro, Q.L., Masieillo, C., Mastrian, S.D., McCloskey, J.C., McDowell, J.J., Pearson, R., Snyder, B., Stantripop, S., Thomas, P.J., Tiogson, E.E., Touchman, J.W., Tsurgeon, C., Vogt, J.L., Walker, M.A., Zhang, L.-H. and Green, E.D.		
	Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at: http://Image.LINL.gov Series: ITAL plate: 15 Row: f Column: 13 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA g1: 3687842. Location/Qualifiers		
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	/db_xref="LocusID:8817"		
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	/clone="MGC:10529 IMAGE:3948893"		
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	/lab_host="DH10B-R"		
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	BASE COUNT	308	a 319 c 343 g 193 t
	ORIGIN		
	Query Match	73.2%	Score 1149.2; DB 9; Length 1163;
	Best Local Similarity	99.3%	Pred. No. 9e-179;
	Matches	1154;	Conservative 0; Mismatches 8; Indels 0; Gaps 0;
	Qy	398	GCGAGCAGTCGAGCAGGGAGGCCGGAGGGAGGAGCAGAGCAGAGGGGGGGCG 457
	Qy	458	GCGCGGGGGGGGGAGGGGCCGGTCCGGCGGCCGGAGGGACACTGGAGGGCG 517
	Qy	62	GCGCGGGGGGGGGAGGGGCCGGTCCGGCGGCCGGAGGGACTGTCGGTGG 121
	CDS		
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	Db	122	GCTAGGAGCGCCSCTCCCTCCGCCAGGATGTTAGCGCCCTCGCCCTCACTT 181
	Qy	578	GCCTGTTTACACTTGCTCTGCTGCTTCAGGTACAGTGTGGT"NGCCGAGGA 637
	Db	182	GCCTGTTTACACTTGCTCTGCTGCTTCAGGTACAGTGTGGT"NGCCGAGGA 241
	Qy	638	ACGTCGACTTCGCACTCACTGGAGAACGAGAGGGCTCGGAGAGGTGAGCCGTA 697
	Db	302	ACGAGCTGGCTGTACAGCTCTAOGCGGACAGTGGAAACACATCAGTCAGGCTG 361
	Db	242	ACGTCGACTTCGCACTCACTGGAGAACGAGACGGGCTCGGAGAGGTGAGCCGTA 301
	Qy	758	GCGGAGGATCAGTCCCCGGGGAGATGGGACAAGTAGTGGCAGCTCTAGTGAGA 817
	Db	362	GCGGAGGATCAGTCCCCGGGGAGATGGGACAAGTAGTGGCAGCTCTAGTGAGA 421
	Qy	878	TGAGCCGAAGGAGCTGTGGGAAGGCCGATGGCACAGTAGTGGCAGCTCTAGTGAGA 937
	Db	482	TGAACCGCAAGGCAGCTGTGGGAAGGCCGATGGCACAGTAGTGGCAGCTCTAGTGAGA 541
	Qy	938	TGAGAGGTTCTGGAGAACACTACACGCCCTGATGTCGGTAAGTAGTACTCCGGCTGGT 997
	Db	542	TCGAGAGGTTCTGGAGAACACTACACGCCCTGATGTCGGTAAGTAGTACTCCGGCTGGT 601
	Db	422	TCGAGAGGTTCTGGAGAACACTACACGCCCTGATGTCGGTAAGTAGTACTCCGGCTGGT 481
	Qy	998	ACGTCGCTTACCAAAGGAGGGGGCCGGAGACGGGACAGTGGCTAAGCTCCGGCTGGT 1057
	Db	602	ACGTCGCTTACCAAAGGAGGGGGCCGGAGACGGGACAGTGGCTAAGCTCCGGCTGGT 661
	Qy	1058	AGGAGCTGATTCTCATGAGGCGTACCCAAAGGGGCCACGGAGCTTCAGAAGGCCCTCA 1117
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	Qy	1298	GAAGACAAACGACCAAAACTCTGGGGGGGGGTGATAAGGATTATGTGAC 1357
	Db	902	GAAGACAAACGACCAAAACTCTGGGGGGGGGTGATAAGGATTATGTGAC 961
	Qy	1358	TGAAACCCCGATGACAAAGACTCACCACCAAGGGACTGTAGTCACCCACAGGTGCT 1417
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	Qy	1418	GTCCTCTCTAGGACACAAACTCTAACCTCGTCCCGAGGAGACTGTAGTGAGGA 1477
	Db	1022	GTCCTCTCTAGGACACAAACTCTAACCTCGTCCCGAGGAGACTGTAGTGAGGA 1081
	Qy	1478	ACCAACTTGTAGGACACCAAGACTCACCACCAAGGGACTGTAGTCACCCACAGGTGCT 1537
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	Qy	1538	AACAAAAAAAGAAAAAA 1559
	Db	1142	AACAAAAAAAGAAAAAA 1163

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LOCUS	AX427499	9						
DEFINITION	Sequence	9						
ACCESSION	AX427499	1						
VERSION	AX427499.1	GT:21537645						
KEYWORDS	human.							
ORGANISM	Homo sapiens							
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;							
AUTHORS	Hodgson, D. M., Lincoln, S. E., Russo, F. D., Spiro, P. A., Banville, S. C., Bratcher, Shawn R., Dufour, G. F., Cohen, H. J., Rosen, B. H., Shah, P., Chalup, M. S., Hillman, J. L., Jones, A. L., Yu, J. Y., Greenawalt, L. B., Panzer, S. R., Roseberry, A. M., Wright, R. J., Chen, W., Liu, T., Yap, P. E., Stockdeler, T. K., Anshay, S., and Fong, W. T.							
TITLE	Molecules for diagnostics and therapeutics							
JOURNAL	Patent: WO 0121836-A 9 29-MAR-2001;							
FEATURES	Incyte Genomics, Inc. (US)							
source	Location/Qualifiers							
BASE COUNT	419	a	424	c	370	g	302	t
ORIGIN	2	others						
Query Match	68.0%		Score	1068;	DB	6	Length	1517;
Best Local Similarity	98.9%		Pred.	No.	1.	9e-165;	Mismatches	0;
Matches	1074;	Conservative					Indels	0;
QY	483	GTCCTCCAGGATACGGGGAGCGGAGATGTCAGGCCCTGGCTAGAGGAGCGCCGCCTCCCTCCCG	542	Db	901	CACGCAAGGGACTGTAGTCACCCAGGGCTGTCCTCCTCTAGGACAGAACACTTCAGGAAACACTTGAGGAAGGCCAAGTC	960	
Db	1	GTCCGGGCGCCGGCGGGAGCGACATGTGAGCTGGCTAGGAGCTCCCTCCCG	60	QY	1443	TAACCTGTCGCCAGAGGAGACTGATGAGGAACACCACACTTGAGGAAGGCCAAGTC	1502	
QY	543	CCAGGAGATACGGCCCTCGGCTGACTGCTTACACTTCCTGCTGCT	602	Db	961	TAACCTGTCGCCAGAGGAGACTGATGAGGAACACCACACTTGAGGAACCCAGTC	1020	
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QY	603	GRGCTTCCAGTACGGTGTGGCCGAGCTGGACTTCGGCATCAGCTGA	662	Db	1021	CTTTTCCCAGAGGAGCTGATGAGGAACCCAGTC	1080	
Db	121	GTGCTTCAGGTACAGTGTGTTGAGGAGAACGCTGGCTCTCCAGCTCA	180	QY	1563	AAAAAA 1568		
QY	663	GAACAGAGACGGCTGGGAGCTGGAGCTGGAGCTGGAGCTGGAGCT	722	Db	1081	GAGAAA 1086		
Db	181	GAACCGAGACGGCTGGGAGCTGGAGCTGGAGCTGGAGCTGGAGCT	240	RESULT	4			
Db	241	CAGCGGGACCGAGCTGGAGAACACATCCAGGCTCTGGCCCGAGGATCAGTGGCTCCCGGGCA	300	AF075291	AF075291			
QY	783	GGATGGGACAAGTATGCCAGCTCTGGAGACAGACCTTGCGTAGTCA	842	LOCUS	AF075291			
Db	301	GGATGGGACAAGTATGCCAGCTCTGGAGACAGACCTTGCGTAGTCA	360	DEFINITION	Mus musculus fibroblast growth factor 18 (Fgf18) mRNA, complete			
QY	843	GATCAGGGCAAGGAGCGGAATTCTACCTGGCTGTGACGCCAAGGAGCTGTGG	902	ACCESSION	AF075291.1			
Db	361	GATCAGGGCAAGGAGACGAATCTACCTGGCTGTGACGCCAAGGAGCTGTGG	420	VERSION	GI:3687840			
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Db	421	GAAGCCGATGGCACCGAGAGGAGTGTGCTGAGCTGAGAGGAGCTGAGA	480	SOURCE	Mus musculus.			
QY	963	CACGCCCTGATGTCGGCTAAGTACTCCGGCTGTACGGGGCTCACCAAGGAGGGGG	1022	ORGANISM	Mus musculus.			
Db	481	CACGCCCTGATGTCGGCTAAGTACTCCGGCTGTACGGGGCTCACCAAGGAGGGGG	540	REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Scuroromathi; Muridae; Mus.			
QY	1023	GCCCCGGAAAGGGCCCAAGCCTGGGAGACCACTGGAGCTGTGCTGAGAAGGCTA	1082	AUTHORS	Hu, M.-T., Oiu, W.R., Wang, Y.-P., Hill, D., Ring, B.D., Scully, S., Bolon, B., Dekose, M., Luethey, R., Simonet, W.S., Arakawa, T. and Danilevko, D.M.			
Db	541	GCCCCGGAAAGGGCCCAAGCCTGGGAGACCACTGGAGCTGTGCTGAGAAGGCTA	600	TITLE	Fgf-18, a novel member of the fibroblast growth factor family, stimulates hepatic and intestinal proliferation			
QY	1083	CCCCAAGGGCACCGGAGCTTCAAGTACACGAGGGTACCAAGAGAGGGTC	1142	JOURNAL	Mol. Cell. Biol. 18 (10), 6063-6074 (1998)			
Db	-	-	MEDLINE	98A14622				
			PUBMED	9742123				
			FEATURES	2 (bases 1 to 1094)				
			source	Hu, M.-T.				
			TITLE	Direct Submission				
			JOURNAL	Submitted (20-JUN-1998) Departments of Cell Biology, Amgen, Inc., One Amgen Center, 1000 Thousand Oaks, CA 91320, USA				
			LOCATION/QUALIFIERS	Location/Qualifiers				
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882	TTGGGAGGGGGCAT-AGGATTCACTGTGACCTGAA--CCCATGACAAGAGCT	937	KGPTRNODVHFMKRYPKQAEIQLQPKFYTIVTKRSRKIRPHEG					
Qy	1383 CACGCAAAGGACTCTAGCACCCACAGGCTGCTGTCCTCTCTAGGACAGACACT	1442						
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Qy	1443 TAACTCGTCCCCAGAGGAGACTGATGAGGAACCAAACACTTGAGAACGCCAAGTC	1502						
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AR088290	AR088290	AR088290	Sequence 1 from patent US 5989866.	917 bp	DNA	linear	PAT 07-SEP-2000	
LOCUS	AR088290	AR088290.1	GI:10015053					
DEFINITION								
ACCESSION								
VERSION								
KEYWORDS								
SOURCE								
ORGANISM								
REFERENCE	1	(bases 1 to 917)						
AUTHORS	Deisher, T.A., Conklin, D.C., Raymond, F., Bukowski, T.R.,							
TITLE	Holderman, S.D., Hansen, B. and Sheppard, P.O.							
JOURNAL								
FEATURES	Patent: US 5989866-A 1 23-NOV-1999;							
source	Location/Qualifiers							
1..917								
BASE COUNT	244	a	/organism="unknown"					
ORIGIN								
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843	GGACGGGAGGAGACAACTGCCCAGCTCTAGTGAGACAGATACCTCTGGGACTCAAGTC	428						
Db	369 GGACGGGAGAAGTATGCCCAGCTCTAGTGAGACAGATACCTCTGGGACTCAAGTC	428						
Qy	843 GATCAGGGAGGAGACGGAACTCTACCTCTAGTGAGACAGATACCTCTGGGACTCAAGTC	902						
Db	429 GATCAGGGAGGAGACAGAACTCTACCTCTAGTGAGACAGATACCTCTGGGACTCAAGTC	488						
Qy	903 GAASCGCGATGGACACCGACAGGAGCTGTTCTAGAAGAGGTCTGAGAACACTA	962						
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Db	762 CGGGCACACTCACCCCGGAGAACACTACATCAGAGGAATTCTACAGGAAATA	821						
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b	1150	ATCGGGCCCAACACCTGCTTAGCCACCCGCCGCGGCCCTCAGGCTGGCC	1209	Db	241	GACAGTAGGCCAGCCTCTAGTGGAGACAGCACCTTCGGTAGTCAAGTGGATAAG	300	
b	601	ATCGGGCCCAACACCTGCTTAGCCACCCGCCGCGGCCCTCAGGCTGGCC	659	QY	850	GCAAGGAGGAAACACATCCAGGCTCGGCCGAGGATCAGTCAGGCTGGCC	909	
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b	660	CACTCACACTCCAGAAACTGATCAGAGGAATTTCATGAAATAAGGAAGAA	708	Db	361	GATGCAACGACATCCAGGCTGGCCGAGGATCAGTCAGGCTGGCC	420	
b	1270	GCTCTATTTGTACATGTTAAAGAGAACAAACTGACCAAACACTCTGGGG	1329	QY	970	CTGATGTCGGCTAAGTACTCGGCTGGTACCTGGCTTACAGGAGGGGGGGGG	1029	
b	709	-	-	Db	421	CTGATGTCGGCTAAGTACTCGGCTGGTACCTGGCTTACAGGAGGGGGGGGG	480	
b	1330	GAGGGGTGATAAGGATTATGTTGACTTGAAACCCCGATGACAAGAACGCAA	1389	QY	1030	AAGGCCCAAGACCGGGGAAACAGCAGCACCTACGGCA	1089	
b	709	-	-	Db	481	AAGGGCCCCAACGACCGGGGAAACAGCAGCACCTACGGCA	540	
b	1390	AGGGACTGTAGTCACCCAGGGCTGTCCTCTCTAGGAAAGACACTCAAC	1449	QY	1090	GGGCAGCCGAGCTTCAGAAGGCCCTCAAGTACAGACGGTACGGCTACCCAG	1149	
b	761	AGGACTGTAGTCACCCAGGGCTGTCCTCTCTAGGAAAGACACTCAAC	820	Db	541	GGGCAGCCGAGCTTCAGAAGGCCCTCAAGTACAGACGGTACGGCTACCCAG	600	
b	1450	GTGCCCAAGAGGAGACTTGATGAGGAACCAACACTTGAGAAACCAAGTCCTTTC	1509	QY	1150	ATCGGGCCACACCCCTGCTTAGGCCACCCGGGGGGGGGGGGGGGG	1209	
b	821	GTGCCCAAGAGGAGACTTGATGAGGAACCAACACTTGAGAAACCAAGTCCTTTC	880	Db	601	ATCGGGCCACACCCCTGCTTAGGCCACCCGGGGGGGGGGGGGGGGGG	659	
b	1510	CCTAAGGTTCTGAAGAAAAAAA	1539	QY	1210	CACTCACCCAGAAACTGATCAGAGGAATTTCATGAAATAAGGAAGAA	1269	
b	881	CCTAAGGTTCTGAAGAAAAAAA	910	Db	660	CACTCACACTCCAGAAACTGATCAGAGGAATTTCATGAAATAAGGAAGAA	708	
b	R198548	-	-	QY	1270	GCTCTATTTGTACATGTTAAAGAGAACAAACTGACCAAACACTCTGGGG	1329	
Y	OCUS	AR198548	-	Db	709	-	-	
Y	DEFINITION	Sequence 1 from patent US 6352971.	917 bp	DNA	linear	PAT 20-APR-2002	708	
Y	ACCESSION	AR198548	1	GI:20248397	QY	1330	GAGGGGTGATAAGGATTATGTTGACTTGAAACCCCGATGACAAGAACGCAA	1389
Y	VERSION	1	-	Db	709	-	-	
Y	KEYWORDS	Unknown.	-	Db	709	-	-	
Y	ORGANISM	Unclassified. 1 (bases 1 to 917)	-	QY	1390	AGGGACTGTAGTCACCCAGGGCTGTCCTCTCTAGGAAAGACACTCAAC	1449	
Y	REFERENCE	Deisher, T.A., Conklin, D.C., Raymond, F., Bukowski, T.R., Holderman, S.D., Hansen, B. and Sheppard, P.O.	-	Db	761	AGGAGCTGTAGTCACCCAGGGCTGTCCTCTCTAGGAAAGACACTCAAC	820	
Y	AUTHORS	Fgf Homologs	-	QY	1450	GTCCCCAGAGGAGACTTGATGAGGAACCAACACTTGAGAAAGCCAAAGTCCTTTC	1509	
Y	TITLE	Patent: US 6352971-A 1 05-MAR-2002;	-	Db	821	GTCCCCAGAGGAGACTTGATGAGGAACCAACACTTGAGAAACCAAGTCCTTTC	880	
Y	FEATURES	Location/Qualifiers 1. .917	-	QY	1510	CCTAAGGTTCTGAAGAAAAAAA	1539	
Y	SOURCE	/organism="unknown"	-	Db	881	CCTAAGGTTCTGAAGAAAAAAA	910	
Y	BASE COUNT	244 a 258 c 252 g 163 t	-	QY	670	ACGGGGCTCGGCCGAGCATGGCGCTTGACGGCTTGACGGCTTGACGGCG	729	
Y	SEQUENCE	Query Match Best Local Similarity 91.6%; Pred No. 2.3e-122; Length 917; Matches 907; Conservative 0; Mismatches 3; Indels 80; Gaps 2;	-	RESULT 7	AX151107	AX151107 Sequence 1 from Patent WO139788.	917 bp	
Y	ACCESSION	550 ATGGTATTTCAGCCCTCGCCCTCACTTGCTTGTTACATTCCTCGCTGGCTTC	609	DEFINITION	LOCUS	DNA	linear	
Y	VERSION	1 ATGATTCAGCCCTCGCCCTCACTTGCTTGTTACATTCCTCGCTGGCTTC	609	ACCESSION	AX151107 AX151107.1 GI:14533309	PAT 22-JUN-2001		
Y	KEYWORDS	human.	-	SOURCE	ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarhini; Hominoidea; Homo.		
Y	610	CGGTACAGGTCTGGTGGCCAGGAGAACGGACTTCGGATCCAGTGGGAACCA	669					
Y	61	CGGTACAGGTCTGGTGGCCAGGAGAACGGACTTCGGATCCAGTGGGAACCA	120					

AUTHORS	West,J.W.
TITLE	Methods for targeting cells that express fibroblast growth receptor 3 or 2
JOURNAL	PATENT: WO 0139788 A 1 07-JUN-2001;
FEATURES	ZymoGenetics, Inc. (US)
Source	Location/Qualifiers 1. .917 /organism="Homo sapiens" 'db_xref="taxon:9606" 1. .624 /note="unnamed protein product" <protein_id="CAC42550_1" <db_xref="GI:1453310" /translation="MYSAPSTCLCLHLFLLCFQVQLVAAEENDFRIVHENQTRAR DVSRLQLRQLQYSITSGRKIQLQVRRIRARGEDDKYVQLLVEDTQSQRTRKG ESEFYLCMRNKGKLPDRJSKECVFIEKVLLENNTALMSAKYSGWYGFKKRGPR KGKPKRNQDVKHNGKPRQKEPFTTIVKRSRKRPTPA"
BASE COUNT	244 a 258 c 252 g 163 t
ORIGIN	
Query Match	51.3%; Score 805.2; DB 6; Length 917;
Best Local Similarity	91.6%; Pred. No. 2.3e-122; Mismatches 0; Indels 80; Gaps 2;
Matches	907; Conservative 0; Mismatches 3; Indels 80; Gaps 2;
Db	709 ----- 708
Qy	1330 GAGGGGTGATAAGGATTATATGTTGACTTGAAACCCCGATGACAACAAAGACTCACCBA 1389
Db	709 ----- 708
Qy	1390 AGGACTGTAGTCACCCACAGGTGCTGTCTCTCTAGGAACAGAACACTCAACTCACCBA 760
Db	761 AGGACTGTAGTCACCCACAGGTGCTGTCTCTCTAGGAACAGAACACTCAACTCACCBA 820
Qy	1450 GTCGCCAGAGGAGCTTGAATGAGGAACCAACACTTGTGAGAAGCCAAGTCCTTTTC 1509
Db	821 GTCCCCAGAGGAGCTTGAATGAGGAACCAACACTTGTGAGAAGCCAAGTCCTTTTC 880
Qy	1510 CCAAAGGTCTGAAAGAAAAAAA 1539
Db	881 CCAAAGGTCTGAAAGAAAAAAA 910
RESULT	8
BB008427	BB008427
LOCUS	Fibroblast growth factor homologs.
DEFINITION	Fibroblast growth factor homologs.
VERSION	BD008427
KEYWORDS	BD008427.1 GI:18636800 JP 200102178-A/1.
SOURCE	unidentified
ORGANISM	unclassified
REFERENCE	(bases 1 to 917)
AUTHORS	Deisher,T.A., Conklin,D.C., Raymond,F.C., BUKOWSKI,T.R., Holderman,S.D., Hansen,B. and Sheppard,P.O.
TITLE	Fibroblast growth factor homologs
JOURNAL	Patent: UP 200102178-A 1 20 FEB 2001;
ZYMOGENETICS INC	
COMMENT	
OS	Unidentified
PN	JP 200102178-A/1
PD	20-FEB-2001
PP	16-OCT-1997 JP 1998518577
PR	16-OCT-1996 US 60/028446
PI	TERESA A DEISHER, DARRELL C CONKLIN, FENELLA C RAYMOND, PI THOMAS R BUKOWSKI,
PI	SUSAN D HOLDERMAN, BRIGIT HANSEN, PAUL O SHEPPARD PC C12N5/18,C07K14/50,C07K16/22,C07K19/00,C12N5/10,A61K38/18 CC
Strandedness:	Double;
CC	Topology: Linear;
FH	Key
FT	Location/Qualifiers
FT	/source
FEATURES	1. .917
Source	/organism="Unidentified"
BASE COUNT	244 a /db_xref="taxon:3264" 258 c 252 g 163 t
ORIGIN	
Query Match	51.3%; Score 805.2; DB 6; Length 917;
Best Local Similarity	91.6%; Pred. No. 2.3e-122; Mismatches 0; Indels 80; Gaps 2;
Matches	907; Conservative 0; Mismatches 3; Indels 80; Gaps 2;
Db	709 ----- 708
Qy	1090 GGGCAGCCGAGCTCAGAACCCCTCAAGTACACCGGTGACAGGTCCCGTCGG 1149
Db	541 GGGCAGCCGAGCTCAGAACCCCTCAAGTACACCGGTGACAGGTCCCGTCGG 600
Qy	1150 ATCCGCCCCAACACACCTCGCTAGGCCACCCCCGGCCGCCCTAGGTGGCC 1209
Db	601 ATCCGCCCCAACACCTCGCTAGGCCACCCCCGGCCGCCCTAGGTGGCC 659
Qy	1210 CACTCACACTCCAGAACACTGCACTGAGGATATTTTACATGAAAGAAAGAA 1269
Db	660 CACTCACACTCCAGAACACTGCACTGAGGATATTTTACATGAAAGAA 708
Qy	670 AGCGGGCTCGGACGATGTGAGCCGATAGAGCTCGGCTACAGCCGG 729
Db	121 AGCGGGCTCGGACGATGTGAGCCGATAGAGCTCGGCTACAGCCGG 180

	JOURNAL	unpublished
	AUTHORS	{bases 1 to 893}
	TITLE	Deisher,T., Conklin,D., Raymond,F., Bukowski,T., Holderman,S.,
	JOURNAL	Hausen,B., Sheppard,P. and O'Hara,P.
Qy	730 ACCAGTGGAAACACATCCAGGCCCTGGCCGAGGATCAGTCCGGCGGGAGGG 789	
Db	181 ACCAGTGGAAACACATCCAGGCCCTGGCCGAGGATCAGTCCGGCGGGAGGG 240	
Qy	790 GACAAGTAGCCAGCTTCAGTGAGACAGACACCTTCGGTAGTCAGTCAGTCAG 849	
Db	241 GACAAGTAGCCAGCTTCAGTGAGACAGACACCTTCGGTAGTCAGTCAG 300	
Qy	850 GGCAGAAGGAGGGAATCTACTCTGTCACTGGAGACAGACACCTTCGGTAGTCAG 909	
Db	301 GGCAGAAGGAGGGAATCTACTCTGTCACTGGAGACAGACACCTTCGGTAGTCAG 360	
Qy	910 GATGGCACCAGCAGGAGGTGTGTCATCGAGAACACTACAGGCC 969	
Db	361 GATGGCACCAGCAGGAGGTGTGTCATCGAGAACACTACAGGCC 420	
Qy	970 CTGATGTCGGCTTAAGTACTCGGCTGTGTTGAGAACACTACAGGCC 1029	
Db	421 CTGATGTCGGCTTAAGTACTCGGCTGTGTTGAGAACACTACAGGCC 480	
Qy	1030 AGGGGCCAACGACCGGGAGACAGAGCAAGAGGGCTACCCAAAGAGGGGGGGGG 1089	
Db	481 AGGGGCCAACGACCGGGAGACAGAGCAAGAGGGCTACCCAAAGAGGGGGGGGG 540	
Qy	1090 GGGCACCGGAGCTTCAGACCCCTCAAGTACAGCACGGTCAAGGCTCCG 1149	
Db	541 GGGCACCGGAGCTTCAGACCCCTCAAGTACAGCACGGTCAAGGCTCCG 600	
Qy	1150 ATCCGCCAACACACCTGCTAGGCCACCCGCCGG-CCTCAGGTCGCC 1209	
Db	601 ATCCGCCAACACACCTGCTAGGCCACCCGCCGG-CCTCAGGTCGCC 659	
Qy	1210 CACTCACACTCCAGAACCTGCTAGAGGATAATTTCACAGAAATAAGAA 1269	
Db	660 CACTCACACTCCAGAACCTGCTAGAGGATAATTTCACAGAA 708	
Qy	1270 GCTCTATTTGTCATGTTAAAGAGACAAACTCTGGGG 1329	
Db	709 ----- 708	
Qy	1330 GAGGGGTATAGGATTATTGTTGACTGAAACCCCCATGACA 1389	
Db	709 ----- 708	
Qy	1390 AGGGACTGTGTCACCCACAGGCTGCTCTCTAGAACACTCTAACTC 1449	
Db	761 AGGGACTGTGTCACCCACAGGCTGCTCTCTAGAACACTCTAACTC 820	
Qy	1450 GTCCCGAGGAGACTGATGAGAACACACTTGAGAACGCCAAGTCCTTTC 1509	
Db	821 GTCCCGAGGAGACTGATGAGAACACACTTGAGAACGCCAAGTCCTTTC 880	
Qy	1510 CCAAAGGTCTGAAAGAAAAAAA 1539	
Db	881 CCAAAGGTCTGAAAGAAAAAAA 910	
RESULT 9		
AF211188 LOCUS AF211188 893 bp mRNA, complete cds.	linear	PRI 04-JAN-2000
DEFINITION Homo sapiens zFGF5 mRNA, complete cds.		
ACCESSION AF211188		
VERSION AF211188.1 GI:6665709		
KEYWORDS		
SOURCE Homo sapiens.		
ORGANISM Homo sapiens.		
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
REFERENCE 1 (bases 1 to 893)		
Deisher,T., Conklin,D., Raymond,F., Bukowski,T., Holderman,S.,		
Hausen,B., Sheppard,P. and O'Hara,P.		
TITLE Homo sapiens homologue of fibroblast growth factor		

Db	601	AACCGGGCCACACACCTGCCCCAGGCCACCCGGG -CCCTCAGGTGCGCTGGCA 659	Db	301	GCGAAGGAGACGGAATTCACCTGFGCATGAACCGCAAAAGCAACTCGTGGGGAGGCC
Qy	1210	CACTCACACTCCAGAACACTCCTACATAGGGATATTTCAGTAAAGAACATAGGAAGA 1269	Qy	910	GATGCCACCGCAGAGGAGTGTGTCTAGAGAAGGTTCTGGAGAACACTACAGGC
Db	660	CACTCACACTCCAGAACACTCCTACATAGGGATATTTCAGTAAAGAACATAGGAAGA 708	Db	361	GATGCCACCGCAGAGGAGTGTGTCTAGAGAAGGTTCTGGAGAACACTACAGGC
Qy	1270	GCTCTAATTTGCTACATGTGTTAAAGAACAGACAAACACTGAACCAAAACTCTGGGG 1329	Qy	970	CTGAGTCGSGCTAACTACTCGGGGTAGTGTGGCTTACCAAGAAGGGGGCGCGG
Db	709	-----	Db	421	CTGAGTCGSGCTAACTACTCGGGGTAGTGTGGCTTACCAAGAAGGGGGCGCGG
Qy	1330	GAGGGGATAGGATTATTTGTTGACTGTAACCCCGATGACAACAAAGACTCACCA 1389	Qy	1030	AAGGCCCAAGACCGGGAGAACAGCAGACACTCTAACCT
Db	709	-----	Db	481	AAGGCCCAAGACCGGGAGAACAGCAGACACTCTAACCT
Qy	1390	AGGGACTGTAGTCACCCACACGGCTGCTCTCTCTAGGACAGAACACTCTAACCT 1449	Qy	1090	GGGGAGCGAGCTCAAGAACCCGGGCTTACAGTACAGAACGGTGTGACCG
Db	761	AGGGACTGTAGTCACCCACACGGCTGCTCTCTCTAGGACAGAACACTCTAACCT 820	Db	541	GGCGGCCAGCTCAGAGCCCTCAAGAACGGTGTGACCG
Qy	1450	GTCGCCAGAGGAGGACTGATGAGGAACACACTTGAGAACAGGAAAGCCTTTTC 1509	Qy	1150	ATCCGGCCACACACCTGCTAGHRANHRSRGIRRGRNNRHNRSRNNAAGCACC
Db	821	GTCCCCAGAGGAGGACTGATGAGGAACACACTTGAGAACAGGAAAGCCTTTTC 880	Db	601	ATCCGGCCACACACACCTGCTAGHRANHRSRGIRRGRNNRHNRSRNNAAGCACC
Qy	1510	CCAAAGGTTCTGA 1522	Qy	1180	CGCGCGCCCTCTAGGTGCGCCACACTCACACCTCCAGAACAAACTGCATCAGAG
Db	881	CCAAAGGTTCTGA 893	Db	661	CGCGCGCCACACACCTGCTAGHRANHRSRGIRRGRNNRHNRSRNNAAGCACC
RESULT 10					
LOCUS	AR140196	AR140196	DEFINITION	Sequence 24 from patent US 6207442.	PAT 16-JUN-2001
ACCESSION	AR140196		VERSION	AR140196.1	GI:14482692
KEYWORDS	Unknown.		SOURCE	Unclassified.	
ORGANISM			REFERENCE	1 (bases 1 to 947)	
AUTHORS	Raymond,C.K.		TITLE	Plasmid construction by homologous recombination	
JOURNAL			FEATURES	Patent: US 6207442-A 24 27-MAR-2001;	
FEATURES	Location/qualifiers		source	1. .947	
BASE COUNT	246	a	/organism="unknown"	258	c
ORIGIN	256	g		163	t
	24	others			
Query Match					
Best Local Similarity	88.9%	Score 48.7%	Score 765.2;	DB 6;	Length 947;
Matches	907;	Conservative	Pred. No. 8.2e-116;	Mismatches	0;
				Indels	3;
				Gaps	110;
					3;
RESULT 11					
LOCUS	AX151109	AX151109	DEFINITION	Sequence 3 from Patent WO0139788.	DNA
ACCESSION	AX151109		VERSION	AX151109.1	GI:14533311
KEYWORDS			SOURCE	house mouse.	
ORGANISM			REFERENCE	Mus musculus	
			AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus;	
			TITLE	1 (bases 1 to 1023)	
JOURNAL			FEATURES	Methods for targeting cells that express fibroblast growth receptor-3 or -2 receptor; ZymoGenetics, Inc. (US) Location/Qualifiers	
FEATURES	source		source	1. .1023	
			/organism="Mus musculus"		
			/db_xref="taxon:10090"		
			1. .624		
			/note="unnamed protein product"		
			/codon_start=1		
			/protein_id="CAC42551.1"		

			/db_xref="GI:1533312"
			/translation="MYSAPACTCLHLFLICFOVQVIAEENVDRIHENQTRAR
			DDVSRQLRLYQLSRSKGKIQVGRIRSARGEDDKYAQOLIVEDFGSQRKGR
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BASE COUNT	321 a	253 c	KGPTRENOQDVMHMKRPRQQAELQPKFVTTVKSRRIRPHG"
ORIGIN	262 g	187 t	
Query Match	47.0%	Score 737.6; DB 6; Length 1023;	
Best Local Similarity	86.6%	Pred. No. 2.7e-111; Mismatches 99; Indels 38; Gaps 5;	
Matches	885;	Conservative 0; Mismatches 99; Indels 38; Gaps 5;	
Qy	550	ATGATATCAGGCCCTCGCCGACTGCACTTGCTGTGTTACACTTCCTGCTGTGCTTC	609
Db	1	ATGATATCAGGCCCTCGCCGACTGCACTTGCTGTGTTACACTTCCTGCTGTGCTTC	60
Qy	610	CAGGTACAGGCTGCTGGCAGAGAAGCTGGACTTCCCATCACGGAGAACAG	669
Db	61	CAGGTACAGGCTGCTGGCAGAGAAGCTGGACTTCCCATCACGGAGAACAG	120
Qy	670	ACGGGGCTGGGACATGAGCTGGCTTAAGGACTGGCTGGCTGTGAGCTCTACGGCG	729
Db	121	ACGGGGCTGGGACATGAGCTGGCTTAAGGACTGGCTGGCTGTGAGCTCTACGGCG	60
Qy	730	ACCACTGGAAACACATCCAGGCGCCAGGATCAGTGGCTGGCGCTGTGAGCTGG	789
Db	181	ACCACTGGAAACACATCCAGGCGCCAGGATCAGTGGCTGGCGCTGTGAGCTGG	240
Qy	790	GACAGTATGCCCAGCTCTTAGTGGAGACAGAACACTTCGGTGAAGTCAGTGGCTCAAG	849
Db	241	GACAGTATGCCCAGCTCTTAGTGGAGACAGAACACTTCGGTGAAGTCAGTGGCTCAAG	300
Qy	850	GGCAAGGAGGAGGAATCTACTTGTGATGACCCGAAAGCAAGCTGGGGAGGCC	909
Db	301	GGCAAGGAGGAGGAATCTACTTGTGATGACCCGAAAGCAAGCTGGGGAGGCC	360
Qy	910	GATGGCACCAGAACAGTGTGTCATGAGAACACTACAGGCC	969
Db	361	GATGGTACTAGCAAGAGTCGGTGTGTCATGAGAACACTACAGGCC	420
Qy	970	CTGATGTGGCTTAAGTACTCGCGCTGGTAGCTGGCTTCAACAGAAAGGGGGG	1029
Db	421	CTGATGTGGCTTAAGTACTCGCGCTGGTAGCTGGCTTCAACAGAAAGGGGGG	480
Qy	1030	AAGGCCGCCAGAACCGGGAGAACCGAGCGAGCTGCAAGGCTACCCAG	1089
Db	481	AAGGCCGCCAGAACCGGGAGAACCGAGCTGCAAGGCTACCCAG	540
Qy	1090	GGCCGCCGAGCTGAGGCCCTAACGAGCTAACGAGCTGGCTGG	1149
Db	541	GGCAGAGGCCGAGCTGAGGCCCTAACGAGCTAACGAGCTGGCTGG	600
Qy	1150	ATCCCGCCACACCGCTGCTAGGCCACCCCCGGCGGCCCTCAGGTGGCC	1209
Db	601	ATCCCGCCACACCGCTGCTAGGCCACCCCCGGCGGCCCTCAGGTGGCC	633
Qy	1210	CACTCACACCCAGAAAACCTGATCAGGAAATTTCATGAAATAAGGAGA	1269
Db	634	CACTCACACCCAGAAAACCTGATCAGGAAATTTCATGAAATAAGGAGA	693
Qy	1270	GCTCTATTGTTGATCAGTGTAAAGAACGAAACTGACCAAACCTGGGG	1329
Db	694	TCTCTATTGTTGATCAGTGTAAAGAACGAAACTGACCAAACCTGGGG	753
Qy	1330	GAGGGGTATAAGGATTATTGTGACTGTAAAGAACGAAACTGACCAA	1389
Db	754	GAGGGGTATAAGGATTATTGTGACTGTAAAGAACGAAACTGACCAA	89
Qy	1390	AGGGACTGTGACTACCCAGGGCTCTCTCTCTGAGAACGAAACTGACCAA	1449
Db	810	GGGAGCCGCTGTCACCCAGAGCTGCTCTCTCTGAGAACGAAACTGACCAA	869
Qy	1450	GTCCCCAGAGGAGACTGAAATGAGAACACACACTTGAGAGCCAAAGTC	1508
BASE COUNT	260 a	248 c	
ORIGIN	253 g	185 t	
Query Match	44.6%	Score 700.2; DB 10; Length 946;	
Best Local Similarity	86.2%	Pred. No. 3.7e-105; Mismatches 98; Indels 38; Gaps 5;	
Matches	847;	Conservative 0; Mismatches 98; Indels 38; Gaps 5;	
Qy	550	ATGATATCAGGCCCTCCGCCTGACTTCCTGCTGTGCTTC	509
Db	1	ATGATATCAGGCCCTCCGCCTGACTTCCTGCTGTGCTTC	60
Qy	610	CAGGTACAGGCTGCTGGTGTGAGGAGACTGGACTTCGCTACCTGGAGAACAG	669
Db	61	CAGGTACAGGCTGCTGGTGTGAGGAGACTGGACTTCGCTACCTGGAGAACAG	120
Qy	670	ACGGGGCTGGAGGATGAGCTGGCTGGAGGAGCTGGCTGTGAGCTGGAGGAGCTGG	729
Db	121	ACGGGGCTGGAGGATGAGCTGGCTGGAGGAGCTGGCTGTGAGCTGGAGGAGCTGG	180
Qy	730	ACCACTGGAAACACATCCAGGCTGGCTGGAGGAGCTGGCTGTGAGCTGGAGGAGCTGG	789
Db	181	ACCACTGGAAACACATCCAGGCTGGCTGGAGGAGCTGGCTGTGAGCTGGAGGAGCTGG	240
Qy	790	GACAGTGTGAGGCCAGCTCTGAGAACGAAACTGACCAAACCTGGAGGAGCTGGAGGAGCTGG	849
Db	241	GACAGTGTGAGGCCAGCTCTGAGAACGAAACTGACCAAACCTGGAGGAGCTGGAGGAGCTGG	300
Qy	850	GGCAGGAGCCGAACTCTACCTGTGATGACCCGAAAGGCAAGCTGGGGAGGCC	909

COMMENT	On Feb 26, 2002 this sequence version replaced gi:7711496. Draft sequence produced by DOE Joint Genome Institute www.jgi.doe.gov
b	910 GATGGCACCAGCAAGGAGTGTGTCTCATCGAGAAGGTTCTGGAGAACACTACAGGCC 969
b	361 GATGGTACTAGCAGGAGTGCGTGTCTGAGGAGGTCTGGAAACACTACAGGCC 420
b	970 CTGATGTTGGCTTAAGTACTCCGCTGTCAGCTGGCTCACAGAAGGGGGGGGG 1029
b	421 CTGATGTTGGCTGCAAGTACTCTGGTTGATGTTGGCTCACAGAAGGGGGCTCGC 480
b	1030 AAGGGCCCCAAGACCCGGAGAACCGAGGACGTGCAATTATGAGGCTTACCCAG 1089
b	481 ANGGTCCCAAGACCCGGAGAACCGAGAATGTCAGTCACTTCATGAAGGGTACCCAG 540
b	1090 GGCGAGCGAGCTCAGAGCCACCCCTGGCCACCGCAGCGGCCCTAGGTGCCCTGGCA 1149
b	541 GAGCAGGCCAGCTGCAGAGCTTCAATAACACACAGTACCGAACGCTACCGGCC 600
b	1150 ATCCGGCCACACCCCTGGCCACCGCAGCGGCCCTAGGTGCCCTGGCA 1209
b	601 ATCCGGCCACACTACCCGGCTAGG----- -TCGGCCA 633
b	1210 CACTCACACTCCAGAAACTGATCAGAGGAATTTTACATGAAATAAGGAGAA 1269
b	634 CACTCACCCCCAGAGAACTACATCAGAGGAATTTCATGAAATAAGGAGAA 693
b	1270 GCCTATTTTGTGACATGTTAAAGAGAACAAACTCTGGGG 1329
b	694 TCTCTATTTTGTACATGTTAAAGAGAACAAACTGAACCTAACGCTTGGGAG 753
b	1330 GGGGGTGTATAAGATTTATGTTGACTGAAACCCGGATGACAAGACTCACCAA 1389
b	754 GAGGGGAT-AGATTCCACTGTGACTCTGA--CCCCTGACAAAGACTCACCAA 809
b	1390 AGGACTGTAGTAGACCACAGGGCTGCTCTCTAGGAGAACACACTAAC 1449
b	810 GGGGACCCGTCAACCCAGGGCTGCTCTCTAGGAGGTGACAACTCAAC 869
b	1450 GTGCCAGGGAGACTGTGATGAGAACCAACACTTGTAGGAAAGCCAAAGTCCTT 1508
b	870 ATGCCAGGGAGACTGTGACCGAGGAA---ACTGCAGAACCAAGTCCTTCCC 923
b	1509 CCCAAGGTCTGAAAGGAAA 1531
b	924 CCCAAAGGTCTGAAAGCAACA 946
RESULT 13	
ORGANISM	Homo sapiens
DEFINITION	Homo sapiens chromosome 5 clone CTB-31E20, complete sequence.
ACCESSION	AC011400
VERSION	5
KEYWORDS	HTG.
SOURCE	Homo sapiens.
Db	160378 bp DNA linear PRI 26-FEB-2002
Db	158056 TTGGGGAGGGGTGATAAGGATTATGTTGACTTGAAACCCGGATGACAAAGACT 157997
Db	158296 CCCCAAGGGCAGCGGAGCTCGAGACGCCCTCAGTACACGAGGTGACAGGGTC 158337
Db	158356 GCGCGGAAGGGGCCAGACCCGGAGACCGAGGACTGATTCATGAGGGCTA 158297
Qy	903 GAAGCCGATGGGACCGAAGGAGTGTGTGTTATCGAGAGGGTCTGGAGAACACTA 962
Db	158416 CAQGGCCCTGATGTGCTTAAGTACTCTCGCTGGTGTACCGAGAACACTA 158417
Qy	963 CACGCCCTGTATGCGTAAGTACTCTCGCTGTTACAGAGGGCTTACCGAGAACGGCG 1022
Db	158416 CAQGGCCCTGATGTGCTTAAGTACTCTCGCTGGTGTACCGAGAACACTA 158357
Qy	1023 GCGCGGAAGGGCCAGACCCGGAGACCGAGGACACCTAAC 1082
Db	158356 GCGCGGAAGGGGCCAGACCCGGAGACCGAGGACTGATTCATGAGGGCTA 158297
Qy	1083 CCCCAAGGGCAGCCGACCTCTAGAAGGCCCTCAAGTACACGAGGTGACAGGGTC 1142
Db	158236 CCCTCGGATCCGGCCACACCCCTGCTAGGCCACCCGGCGGCCCTCAGTCGCC 158177
Qy	1203 CTGGCCACTCACCTCCAGAAACCTGATCAGAGGAATTTTACGAAATAA 1262
Db	158176 CTGGCCACTCACCTCCAGAAACCTGATCAGAGGAATTTTACGAAATAA 158117
Qy	1263 GGAGAAGCTCTATTTTGTACATGTTAAAGAGAACAAACTGACCAAAACTC 1322
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REFERENCE	1	(bases 1 to 175154)
AUTHORS		DOE Joint Genome Institute and Stanford Human Genome Center.
TITLE		Direct Submission
JOURNAL		Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94558, USA
REFERENCE	3	(bases 1 to 175154)
AUTHORS		DOE Joint Genome Institute.
TITLE		Submitted (18-DEC-2001) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94558, USA
COMMENT		On Dec 18, 2001 this sequence version replaced gi 15290460.
		Draft Sequence Produced by DOE Joint Genome Institute
		www.jgi.doe.gov
		Finishing completed at Stanford Human Genome Center
		www.shgc.stanford.edu
FEATURES		Quality: phrap Quality >=40 99.3% of Sequence;
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QY	1143	CGCGCGGATCCGCCAACACACCCCTGCCTAGGCCACCCCCGGGGCCCTAGGTGCC 1202
DO	38297	_ CGCGCGGATCCGCCAACACACCCCTGCCTAGGCCACCCCCGGGGCCCTAGGTGCC 38238
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REFERENCE	1	Kreutzer, R., Limmer, S., Rost, S. and Hadwiger, P.
AUTHORS		Method for inhibiting the expression of a target gene
TITLE		Patent: WO 20055693-A 61 18-JUL-2002;
JOURNAL		Ribopharma AG (DE)
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